



SYED FARHAN AHMAD

Ph.D.



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EDUCATION

- 2019 Postdoctoral researcher (Genome informatics) Kasetsart University, Thailand
- 2018 Visiting researcher scholar (Genomics and informatics) University of Connecticut, USA
- 2019 Ph.D. (Genetics) Sao Paulo State University, Brazil
- 2013 MS (Biotechnology) International Islamic University Islamabad, Pakistan
- 2005 BS (Biotechnology), 1st honor University of Malakand, Pakistan

EMPLOYMENT HISTORY

- 02/2020-present Postdoctoral researcher Kasetsart University, Thailand
- 08/2018 – 02/2019 Visiting research scholar, University of Connecticut, USA
- 03/2015 – 05/2019 Sao Paulo Research Foundation, (FAPESP) fellowship holder
- 06/2013 – 01/2015 Biology lecturer, Iqra College of Science, Pakistan

ENGLISH LANGUAGE ELIGIBILITY

Qualified English proficiency examination TOFL Kasetsart University (Test: KU-EPT 2563/10 All) with **78.75 % Average score.**

Test Date: Sun, 23 Aug. 2020

Test Time: 13:00-16:00

RESEARCH INTERESTS

I am a biologist with specialization in genome informatics. I developed my research interest and advanced training in bioinformatics, chromosomics and evolutionary genomics. I have experience in cytogenomics, NGS data processing, genome assemblies, comparative and population genomics. I have plans to work on the following research topics:

1. Whole genome sequencing, de novo assemblies and annotation of vertebrates

To sequence the genomes of diverse vertebrates' species and assemble these genomes for studying different genetics aspects and enhance understanding on genome evolution. To generate sequencing data and utilize this data for efficient development and advancement of animal breeding program.

2. Genome informatics applied to Bioresources management

To generate genome reference resources of biological and agricultural vital animal species with application of multiple omics and advanced bioinformatics technologies. During my postdoc position I have been involved in several genome projects of economically and culturally important animal species such as Betta, chicken and macaque's genomics. The application of genome technology and informatics as a modern tool will allow agricultural innovation and better sustainability of animal bioresources.

3. Comparative genomics of vertebrates

To elucidate the process of genome evolution in vertebrates, the chromosome homologies between different species in fish, amphibians, reptiles, birds and mammals are deduced using comparative genomics.

4. Chromosomics: Origin and evolution of sex chromosomes in vertebrates

Mammals and birds have a male heterogametic XX/XY-type sex chromosome, and a female heterogametic ZZ/ZW-type sex chromosome, respectively, whereas amphibians have both XX/XY- and ZZ/ZW-type sex chromosome. By contrast, XX/XY- and ZZ/ZW-type sex chromosome not only co-exist in reptiles and fish as genetic sex determination, but the environmental sex determination such as temperature is also found in both vertebrate groups. To clarify the origin and differentiation of sex chromosomes, the comparative chromosome maps of sex chromosomes are constructed and compared them with other species. Furthermore, sex-determining genes such as *DM* and *SOX* family are proposed to be a candidate gene of sex determination in vertebrates. The orthologues and paralogues of sex-determining gene, therefore, are studied to disclose gene evolution in vertebrate.

5. Organization of repetitive element in vertebrate genome

Repetitive DNA sequences is a good chromosome marker for investigating the process of karyotypic evolution and sex chromosome identification, and for comparing the genomics structure of vertebrate species. This can be also a source for homologous recombination to initiate various categories of chromosomal rearrangements. Here, the characterization and comparison of organized repetitive element among different species should be conducted to find the common and specific repeats in the evolutionary line.

6. Population genomics and Genetic diversity

To clarify the step of evolution and population demography in vertebrates, genome wide SNP, mitochondrial genome and nuclear gene analyses is used. The structure and organization are compared among different species within the same class or among population within the same species. The data sets are also scrutinized through cladistic analysis to demonstrate the genetic and genomic diversity among them.

COURSES (TEACHING INTEREST AND AREA OF EXPERTISE)

I am interested to advance my teaching skills in the following subjects.

- Bioinformatics
- General Biology
- Cell Biology
- Chromosomics
- Research Technique in Genetics
- Genome informatics and Linux
- Molecular Biology
- Genetic Engineering
- Biotechnology Applications

AWARDS AND RESEARCH FUNDING

(2021) Best Postdoc presentation award, International chromosome conference (ICC & ICACG)

(2014) Selected for TWAS postgraduate fellowships (US\$ 30,000)

(2015 - 2019) FAPESP PhD fellowship (US\$ 50,000)

(2018-2019) FAPESP research exchange fellowship (\$12,000)

(2017 - 2020) Thematic Grand project: Sex and B chromosomes enigmas:

FAPESP (participant), (\$100,000)

RESEARCH SKILLS AND EXPERTISE

Bioinformatics:

- Use of computer clusters and servers
- R (Bioconductor), Bash (linux), Basic level Python for processing, and statistical analysis of NGS short and long reads data
- Deep theoretical and practical knowledge of long reads (PacBio, Nanopore) and short reads (Illumina) sequencing and data management, quality evaluation and data analysis skills with bioinformatics
- Comparative genomic (Whole genome alignments, synteny analysis)
- Genome assemblies
- Identification of genetic polymorphism and mutations
- Structural variations and rearrangements analysis of genomes
- Genes annotation and Repeatomes analysis
- Experienced in bioinformatic tools, including: Bowtie 2, BWA, minimap2, Circos, Samtools, GATK, Bedtools, MUGSY, MUSCLE, SoapDenovo, Velvet, MAKER, BLAST2GO, VCFtools, Picard, RepeatMasker, RepeatExplorer, FASTXtoolkit, Geneious
- Infographics design: InkScape and SVG production, R studio,

Molecular Biology and Cytogenetics:

- DNA/RNA extraction
- Gel electrophoresis
- Sequencing libraries preparation
- qPCR
- Florescent Insito Hybridization (FISH)

PUBLICATIONS

- 1) Nguyen DHM, Ponjarat J, Laopichienpong, N Kraichak E, Singchat, W, **Ahmad SF**, et al. 2020. Genome-wide SNP analysis suggests male heterogamety in bighead catfish (*Clarias macrocephalus*, Günther, 1864). *Aquaculture*, 543, (IF (2020) = 3.224) Publisher: Elsevier, <https://doi.org/10.1016/j.aquaculture.2021.737005>.
- 2) **Ahmad SF**, Singchat W, Panthum T, and Srikulnath K. 2021. Impact of repetitive DNA on snake genome biology and evolution. *Cells*. 10, (IF (2021) = 6.6). <https://doi.org/10.3390/cells10071707>.
- 3) Thintip J, **Ahmad SF**, Singchat W. et al. 2020. Mitochondrial genome of bronze-winged jacana (*Metopidius indicus*, Latham 1790). **Mitochondrial DNA Part B**, in press, (IF (2019) = 0.885)

(SCI-E) (Scopus) Publisher: Taylor & Francis (†Equal first author).
<https://pubmed.ncbi.nlm.nih.gov/33796646/>

- 4) **Ahmad SF**, Jehangir M, Srikulnath, and Martins C. Fish genomics and its impact on vertebrate biology. (under review in Reviews in Fish Biology and Fisheries)
- 5) Ariyaraphong N, Pansrikaew T, Jangtarwan K, Thintip J, Singchat W, Laopichienpong N, **Ahmad SF**, et al. 2021. Introduction of wild Chinese gorals into a captive population requires careful genetic breeding plan monitoring for successful long-term conservation. **Global Ecology and Conservation**, 28, (IF (2021) =3.380), Publisher: Elsevier, <https://www.sciencedirect.com/science/article/pii/S2351989421002250#>!
- 6) Ariyaraphong N, Laopichienpong N, Singchat W, Panthum T, **Ahmad SF**, et al. 2021. High-Level Gene Flow Restricts Genetic Differentiation in Dairy Cattle Populations in Thailand: Insights from Large-Scale Mt D-Loop Sequencing. **Animals**. (IF (2021) =2.758), Publisher: MDPI
- 7) **Ahmad SF**, Singchat W, Jehangir M, Suntronpong A, Panthum T, Malaivijitnond S, and Srikulnath K. 2020. Dark matter of primate genomes: satellite DNA repeats and their evolutionary dynamics. **Cells**. 9(12), 2714; (IF (2019) = 5.656) (SCI-E) (PubMed) Publisher: MDPI, <https://doi.org/10.3390/cells9122714>
- 8) **Ahmad SF**, Jehangir M, Cardoso AL, Wolf IR, Margarido, VP, Cabral-de-Mello DC; O'Neill RJ, Valente GT, Martins C. 2020. B chromosomes of multiple species have intense evolutionary dynamics and accumulated genes related to important biological processes. **BMC Genomics**. 21, 656 (IF (2019) = 3.594). <https://doi.org/10.1186/s12864-020-07072-1>
- 9) Srikulnath K, Singchat W, Laopichienpong N, **Ahmad SF**, et al. 2021. Overview of the betta fish genome regarding species radiation, parental care, behavioral aggression, and pigmentation model relevant to humans. **Genes Genomics**. 43(2):91-104. (IF (2019) = 1.188) (SCI-E) (PubMed) Publisher: Springer
- 10) Nguyen DHM, Panthum T, Ponjarat J, Laopichienpong, N Kraichak E, Singchat, W, **Ahmad SF**, Muangmai N, Peyachoknagul S, Na-Nakorn U, and Srikulnath S. 2020. An Investigation of ZZ/ZW and XX/XY sex determination systems in North African catfish (*Clarias gariepinus*, Burchell, 1822). **Frontiers in Genetics**. 11: 948. (IF (2019) = 3.258) (SCI-E) (PubMed) Publisher: Frontiers. doi: 10.3389/fgene.2020.562856
- 11) Singchat W, **Ahmad SF**[†], Laopichienpong N, Suntronpong A, Panthum T, Griffin DK, Srikulnath, K. Snake W Sex Chromosome: The Shadow of Ancestral Amniote Super-Sex Chromosome. **Cells**

2020, 9, 2386. (IF (2019) = 5.656) (SCI-E) (PubMed) Publisher: MDPI (†Equal first author).
<https://pubmed.ncbi.nlm.nih.gov/33142713/>

- 12) Koomgun T, Laopichienpong N, Singchat W, Panthum T, Phatcharakullawarawat R, Kraichak E, Sillapaprayoon S, **Ahmad SF** et al. 2020. Complexity Reduction High-Throughput Genome Sequencing of Green Iguana (*Iguana iguana*) Reveal a Paradigm Shift in Understanding Sex-Chromosomal Linkages on Homomorphic X and Y Sex Chromosomes. **Frontiers in Genetics**. 11: 948. (IF (2019) = 3.258) (SCI-E) (PubMed) Publisher: Frontiers.
<https://www.frontiersin.org/articles/10.3389/fgene.2020.556267/full>
- 13) **Ahmad SF**, Laopichienpong N, Singchat W. et al. 2020. Next-generation sequencing yields complete mitochondrial genome assembly of peaceful betta fish, *Betta imbellis* (Teleostei: Osphronemidae). **Mitochondrial DNA Part B**, (IF (2019) = 0.885) (SCI-E) (Scopus) Publisher: Taylor & Francis. <https://www.tandfonline.com/doi/full/10.1080/23802359.2020.1841582>
- 14) Laopichienpong N, **Ahmad SF**[†], Singchat W. et al. Complete mitochondrial genome of Mekong fighting fish, *Betta smaragdina* (Teleostei: Osphronemidae). **Mitochondrial DNA Part B**, in press, (IF (2019) = 0.885) (SCI-E) (Scopus) Publisher: Taylor & Francis (†Equal first author).
<https://pubmed.ncbi.nlm.nih.gov/33796646/>
- 15) Singchat W, **Ahmad SF**, Sillapaprayoon N, Muangmai S, Baicharoen C, Indananda P, Duengkae S, Peyachoknagul RE, Connor O, Griffin D and Srikulnath K. 2020. Partial amniote sex chromosomal linkage homologies shared on snake W sex chromosomes support the ancestral super-sex chromosome evolution in amniotes. **Frontiers in Genetics**. 11: 948. (IF (2019) = 3.258) (SCI-E) (PubMed) Publisher: Frontiers. <https://doi.org/10.3389/fgene.2020.00948>
- 16) **Ahmad SF**, Singchat W, Jehangir M, Panthum T, Srikulnath K. 2020. Consequence of Paradigm Shift with Repeat Landscapes in Reptiles: Powerful Facilitators of Chromosomal Rearrangements for Diversity and Evolution. **Genes**, 11, 827. (IF (2019) = 3.759) (SCI-E) (PubMed) Publisher: MDPI. <https://doi.org/10.3390/genes11070827>
- 17) Singchat W, **Ahmad SF**[†], Laopichienpong N, Suntronpong A, Pongsanarm T, Panthum T, Ariyaraphong N, Subpayakom N, Dokkaew S, Muangmai N, Duengkae P, Srikulnath K (2020) Complete mitochondrial genome of Mahachai betta, *Betta mahachaiensis* (Teleostei: Osphronemidae), **Mitochondrial DNA Part B**, 5:3, 3077-3079. (IF(2019) = 0.885) (SCI-E) (Scopus) Publisher: Taylor & Francis <https://doi.org/10.1080/23802359.2020.1797578> (†Equal first author)

- 18) **Ahmad SF** and Martins C. The modern view of B chromosomes under the impact of high scale omics analyses. **Cells** 8(2): 156 (2019) (IF (2018) = 5.656) (SCI-E) (PubMed) Publisher: MDPI <https://0-www-ncbi-nlm-nih-gov.brum.beds.ac.uk/pubmed/30781835>
- 19) Jehangir M, **Ahmad SF**, Cardoso AL, Valente GT, Ramos E, Martins, C. De novo genome assembly of the cichlid fish *Astatotilapia latifasciata* reveals a higher level of genomic polymorphism and genes related to B chromosomes. **Chromosoma** 128:81–96 (2019). (IF (2018) = 4.4) (SCI) (PubMed) Publisher: Springer
- 20) Jehangir I, **Ahmad SF**, Jehangir M, Jamal A, and Khan M. Integration of bioinformatics and in vitro analysis reveal anti-leishmanial effects of azithromycin and nystatin. **Current Bioinformatics** 14:1-10 (2019)(IF (2018) = 2.068) (SCI-E) (Scopus) Publisher: Bentham Science Publisher <https://doi.org/10.2174/1574893614666181217142344>
- 21) **Ahmad SF**, Jehangir, Anwar Z, Hussain S, Jehangir M, Jehangir I, Jamal A, et al . A detailed report on the specific area-based percentage and diagnostic methods of hepatitis C in Khyber Pakhtunkhwa, Pakistan. **Molecular and Biochemical Diagnosis Journal** 2 (1) :51-64 (2016) (Semantic scholar) Publisher: Tarbiat Modares University Press. <http://journals.modares.ac.ir/article-8-10543-en.pdf>
- 22) Jehangir M and **Ahmad SF**. Structural Studies of Aspartic Endopeptidase pep2 from *Neosartorya fisherica* Using Homolgy Modeling Techniques. **International Journal on Bioinformatics & Biosciences** 3: 7-20 (2013). (ProQuest) Publisher: Wireilla Scientific Publications <https://wireilla.com/papers/ijbb/V3N1/3113ijbb02.pdf>
- 23) **Ahmad SF**, Jehangir M, Hameed A, Khattak, J.ZK. Molecular study of a consanguineous family with autosomal recessive mental retardation and speech disorder. **Molecular Biology and Research Communication**. 1: 83-93 (2012) (PubMed: 2322-181x) Publisher: Shiraz University. http://mbrc.shirazu.ac.ir/article_1098_57cee48c0ee9da2b4b59496b01369a9f.pdf
- 24) Anwar Z, Hussain S, **Ahmad SF**, Khan AA, Jamil T, Qadir SM, Lodhi AF, Khattak, JZK. Prevalence of Hepatitis B detected through RT PCR in Khyber Pakhtunkhwa. **African Journal of Microbiology Research**, 6: 3631-3634 (2012) (Google Scholar) <https://academicjournals.org/journal/AJMR/article-full-text-pdf/92E870E29724>

- 1) Ahmad SF and Srikulnath K. Siamese cobra genome and evolutionary trajectories of chromosomes rearrangements. 23rd International Chromosome Conference (ICC) and the 24th International Colloquium in Animal Cytogenetics and Genomics (ICACG). 13th to 17th July 2021. *Talk*.
- 2) **Ahmad SF**, Malaivijitnond S and Srikulnath K. Population genomics analysis provides new insights into genetic admixture and diversity of rhesus and long-tailed macaques. The 1st Symposium of the Natural History Museum, National Science Museum Thailand. 24-25 September 2020. *Oral presentation*
- 3) **Ahmad SF**, Martins C. The impact of omics analyses in the modern view of B chromosomes. **4th B Chromosome Conference**, (BCC), Botucatu, Brazil. 20 - 23 July 2019. *Oral presentation*
<https://link.springer.com/content/pdf/10.1186%2Fs12919-019-0165-x.pdf>
BMC Proceedings, 13, 2019, (IF (2018) = 0.74) Publisher: Springer
- 4) **Ahmad SF**, Cabral-de-Mello DC, Parise-Maltempo P, Margarido VP , O'Neill R, Valente GT, Martins C. The integrative genomics and bioinformatics analysis unveil the genetic contents and evolutionary origin of B chromosomes. **Conference on Regulatory and system genomics**, International society for computational biology (ISCB) (2018), RSG, New York, USA.
<https://www.iscb.org/recomb-regsysgen2018>
- 5) Martins C, Nakajima RT, Fantinatti B, Marques DF, Venturelli NB, Jehangir M, Ramos E, Oliveira JI, **Ahmad SF**, Cardoso A, Valenti GT. B chromosomes in the light of functional analysis. **23rd International Colloquium of animal cytogenetics and genomics** (23 ICACG) (2018), Saint-Petersburg Russia. Comparative cytogenetics 12: 299–360 (2018) (IF (2018) = 1.31) (SCI-E) doi: 10.3897/CompCytogen.v12i3.274 <http://compcytogen.pensoft.net>
- 6) **Ahmad SF**, Cabral-de-Mello DC, Parise-Maltempo P, Margarido VP , O'Neill R, Valente GT, Martins C. Fishing for B chromosome genes. **XVIII Simpósio de Citogenética e Genética de Peixes (SCGP)** (2018), Cascavel, Brazil. <https://midas.unioeste.br/sgev/eventos/scgp2018>
- 7) Martins C, Nakajima RT, Ramos E, Fantinatti B, Valenti GT, Cardoso A, Jehangir M, Marques DF, Oliveira, JI, Bovolenta IA, Venturelli NB, Kocher TD, **Ahmad SF**. Fishing for B chromosome effects. **22nd Internationale Chromosome Conference(ICC)** (2018), Prague, Czech Republic.
- 8) **Ahmad SF**, Valente GT, Martins C. The distribution of repetitive DNAs between regular and supernumerary chromosomes in the cavefish genome. **The 36th International Society for Animal Genetics Conference (ISAG)** (2016), University College Dublin, Ireland.
<https://www.isag.us/2017/>

- 9) **Ahmad SF**, Jehangir M, Cardoso A, Martins C. FISH mapping of 45S Rrna and Ihhb genes on autosomes and B chromosome of cichlid fish *Astatotilapia latifasciata*. **5th Brazillian meeting of cytogenetics and cytogenomics (2017)**, Londrina, Brazil. <http://rbcc2017.wixsite.com/londrina>
- 10) Jehangir M, **Ahmad SF**, Valente GT, Martins C. A coverage based study of Ihhb and 45S RNA genes in the B chromosomes of *Astatotilapia latifasciata* to highlight polymorphism levels. **21st International Chromosome Conference (ICC) (2016)** Foz do Iguacu, Brazil. Cytogenetic and Genome Research 148. p. 83-155. (2016) (IF (2018) = 1.58) (SCI-E) DOI: 10.1159/000446523 <https://www.karger.com/Article/Pdf/446523>
- 11) **Ahmad SF**, Valente GT, Jehangir M, Coan R, Martins C. Genomic Analysis of Transposable Elements in *Astyanax correntinus* with focus on B Chromosome. 21st International Chromosome Conference (ICC) (2016) Foz do Iguacu, Brazil. Cytogenetic and Genome Research 148: 83-155 (2016) (IF (2018) = 1.58) (SCIE) DOI: 10.1159/000446523 <https://www.karger.com/Article/Pdf/446523>
- 12) Jehangir M, **Ahmad SF**, Valente GT, Ramos E, Fantinatti B, Martins C. Assembly of the cichlid fish *Astatotilapia latifasciata* genome with focus in B chromosome. **61 Congresso Brasileiro de Genética (2015)** Águas de Lindoia, Brazil. <https://www.sbg.org.br/en>
- 13) **Ahmad SF**, Valente GT, Martins C. Searching for transposable elements in the genome of cavefish *Astyanax mexicanus*. 61 Congresso Brasileiro de Genética (2015) Águas de Lindoia, Brazil. <https://www.sbg.org.br/en>